

SEQUENCING PROTOCOL <110> Degussa AG <120> Nucleotide sequences coding for the sigD gene <130> 00044\$ BT <140> <141> <160> 2 Ver. 2.1 <170> PatentIn <210> 1 <211> 1129 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (301)..(864) <223> sigD-Gen <400> 1 catatgcagg cgaactcctg &tagtacgcc cgttctgacc tgcggttatg tgtcgaggtg 60 aatctccggt gaattcttat a@ataacttg tttttgcagg tcaggacggg gttaagggga 120 tgggtgttat ctgtcagtat gt \d aggagat caaggtgttg ggggttctag ttgctaagat 180 ggtgaaaacc cgtgaggcca aaa ψ ccaact gggtgaatta cccctgcata aatgcatgag 240 ggctttatac ttgtcttatt attaaacttt tagggttttg atgcaggaag gtgcgagaac 300 ttg get gat act gag ege gag kte get gae etg gta eeg eag gea aeg Met Ala Asp Thr Glu Arg Glu Aeu Ala Asp Leu Val Pro Gln Ala Thr 396 qcq ggc gat cgt cgg gca ttg ca λ aga ata atg gag att att cac ccc Ala Gly Asp Arg Arg Ala Leu Gln\Arg Ile Met Glu Ile Ile His Pro att gtt ttg cgt tat gct cgc gct cqt att gga ggt gga cgc cag cca 444 Ile Val Leu Arg Tyr Ala Arg Ala Atg Ile Gly Gly Gly Arg Gln Pro acg gca gaa gac gtt gct caa gaa atc\tgc ctg gcg gta gcc acc tcc Thr Ala Glu Asp Val Ala Glu Glu Ile cys Leu Ala Val Ala Thr Ser 492 att agg aac ttt gtc gac cag ggt agg ccg ttc atg gcg ttt gtc tac 540 Ile Arg Asn Phe Val Asp Gln Gly Arg Pro Phe Met Ala Phe Val Tyr 65 ggc att gca tct aac aag gtc gca gat gct ca/c agg gcg atg tcg agg Gly Ile Ala Ser Asn Lys Val Ala Asp Ala Hia Arg Ala Met Ser Arg 90 85

			1														
gat Asp	aaa Lys	tcg Ser	act Thr 100	cct Pro	att Ile	gag Glu	gaa Glu	gtc Val 105	cca Pro	gaa Glu	act Thr	tca Ser	cca Pro 110	gat Asp	act Thr	636	
ttt Phe	acc Thr	ccc Pro 115	gala Glu	gac Asp	ttt Phe	gcg Ala	ctg Leu 120	gtc Val	agc Ser	gat Asp	gga Gly	agt Ser 125	aac Asn	aga Arg	gtt Val	684	
agg Arg	gaa Glu 130	ctt Leu	ctc Leu	gat Asp	cta Leu	ctg Leu 135	agt Ser	gaa Glu	aag Lys	gca Ala	cgc Arg 140	gac Asp	att Ile	ctt Leu	atc Ile	732	
ttg Leu 145	aga Arg	gtt Val	atc Ile	gt Val	ggt Gly 1 50	ctt Leu	tcc Ser	gca Ala	gaa Glu	gaa Glu 155	act Thr	gca Ala	gag Glu	atg Met	gtg Val 160	780	
ggc Gly	agc Ser	acc Thr	cca Pro	ggt Gly 165	gct Ala	gta Val	cga Arg	gtt Val	gcc Ala 170	caa Gln	cac His	agg Arg	gca Ala	ctc Leu 175	acg Thr	828	
aca Thr	ctt Leu	cga Arg	agc Ser 180	aca Thr	ct. Leu	gag Glu	cag Gln	cag Gln 185	gag Glu	aac Asn	aag Lys	ag taatgactcg ys					
acgt	acgtctacat ggtggtgagc aggatggcca ggaacacgtt aaaggacagc taaagcagct															934	
gtto	gttcgacgac gacgcgttct tgactgacct gtcccgcggc gttgatccct cagagggcga															994	
tgad	tgacgccctc gctggcctcc tcctcgattt aacaaaggaa gctcaggagc cgccggcaac															1054	
aatç	aatgccggat tggtctactt tgctccdtgg aattttggat caggatcagg atttgccagt															1114	
ggaatccact tcgga															1129		
<210> 2 <211> 188 <212> PRT <213> Corynebacterium glutamicum																	
<400 Met 1		Asp	Thr	Glu 5	Arg	Glu	Leu	Ala	Asp	Leu	Val	Pro	Gln	Ala 15	Thr		
Ala	Gly	Asp	Arg 20	Arg	Ala	Leu	Gln	Arg 25	lle	Met	Glu	Ile	Ile 30	His	Pro		
Ile	Val	Leu 35	Arg	Tyr	Ala	Arg	Ala 40	Arg	119	Gly	Gly	Gly 45	Arg	Gln	Pro		
Thr	Ala 50	Glu	Asp	Val	Ala	Gln 55	Glu	Ile	Cys	leu	Ala 60	Val	Ala	Thr	Ser		
65			Phe '		70					74					80		
Gly	Ile .	Ala	Ser /	Asn 85	Lys	Val	Ala	Asp	Ala 90	His\	Arg 	Ala	Met	Ser . 95	Arg		

Asp Lys Ser Thr Pro Ile Glu Glu Val Pro Glu Thr Ser Pro Asp Thr 100

Phe Thr Pro Glu Asp Phe Ala Leu Val Ser Asp Gly Ser Asn Arg Val 115

Arg Glu Leu Leu Asp Leu Leu Ser Glu Lys Ala Arg Asp Ile Leu Ile 130

Leu Arg Val Ile Val Gly Leu Ser Ala Glu Glu Thr Ala Glu Met Val 145

Gly Ser Thr Pro Gly Ala Val Arg Val Ala Gln His Arg Ala Leu Thr

Thr Leu Arg Ser Thr Leu Glu Gln Glu Asn Lys
180 185